In the Interview Summary, the examiner recommended "limiting the claims to specific sequences critical regarding the binding pocket." Claims 6 and 7 appear to satisfy that recommendation.

Applicant respectfully inquires whether the examiner meant to reject claims 6 and 7, which relate to specific amino acid structures and *S. pyogenes*. In the Advisory Action, 102(b) and 102(e) art rejections were withdrawn for claim 6. Also 112, 1st paragraph rejections were overcome. Also applicants had the impression the examiner favored allowing those claims with specific coordinates so applicants wonder if at least claim 6 is also allowed. Claim 7 appears to have been allowed based on recommendations of the Office Action of March 22, 2000 (now responded to by amendments to delete "comprise coordinates").

If claims 6 and 7 must also be cancelled for allowance to proceed, applicant agrees.

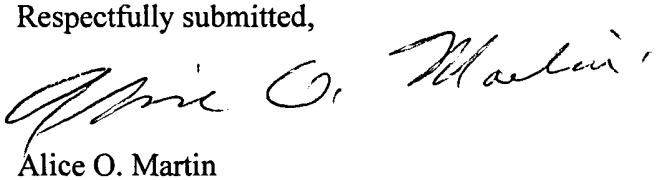
II. Summary and Conclusion

For the reasons stated above, applicant requests allowance of all pending claims.

Please contact applicants' representative if you have any questions.

No other fees are believed due at this time, however, please charge any deficiencies or credit any overpayments to deposit account number 10-0435 with reference to our attorney docket number (21416-90042).

Respectfully submitted,



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MARKED UP VERSION OF CLAIMS
FOR SERIAL NO. 09/533,466

WE CLAIM:

[1. A crystal of IMPDH (ionisine monophosphate dehydrogenase) isolated from a bacterial preparation.]

2. (Amended)The crystal of claim [1] 3 further characterized by ability to provide x-ray diffraction patterns useful to define molecular structures for bacterial IMPDH enzymes.

3. (Amended) [The crystal of claim 1] A crystal of bacterial IMPDH (inosine monophosphate dehydrogenase) isolated from a bacterial preparation wherein the bacterial preparation is a pure culture of *Streptococcus pyogenes*.

4. (Twice Amended) A method for developing lead compounds for an inhibitor of bacterial IMPDH (inosine monophosphate dehydrogenase), said method comprising:

[a.](a) obtaining a crystal of bacterial IMPDH;

[b.](b) recording x-ray diffraction data from said crystal;

[c.](c) using said diffraction data to generate an electron density map consistent with a [the] model for the molecular structure of a binding pocket of IMPDH; and

[d.](d) developing lead compounds for an inhibitor of bacterial IMPDH based on the map of three dimensional structural information of the molecular structure of the binding pocket of IMPDH.

[5. A crystalline molecule or molecular complex comprising an IMPDH binding pocket defined by the structural coordinates of IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-433, and 449-455 according to Table 7 or a homologue of said molecule or molecular complex.]

6. (Twice Amended) A crystalline molecule or molecular complex comprising [all or any parts] of a binding pocket wherein said binding pocket is defined by structure coordinates of IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-432 and 449-455, according to Table 7, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has an amino acid sequence identity for the

MARKED UP VERSION OF CLAIMS
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corresponding binding pocket residues of 60% or greater relative to the *S. pyogenes* IMPDH binding pocket.

7. (Twice Amended) A crystalline IMPDH molecule defined by structural coordinates for IMPDH amino acids [comprising coordinates] from *S. pyogenes* IMPDH amino acids 50-56, 75-80, 229-235, 252-260, 283-286, 302-322, 343-345, 365-433, and 449-455.

[8. A crystalline IMPDH molecule having (inosine monophosphate) IMP in its binding pocket.]